**AMENDMENTS TO THE CLAIMS:**

Please amend claim 1, 9, 16, 17, 22 and 23. This listing of claims replaces all prior versions, and listings of claims, in the application.

**LISTING OF CLAIMS:**

1. (Currently amended) A process for the ~~production~~ identification of a peptide, polypeptide, or protein ~~having a~~ that differs in a predetermined property from a target protein, comprising:

(a) producing a population of sets of nucleic acid molecules that encode modified forms of a target protein;

(b) introducing each set of nucleic acid molecules into host cells and expressing the encoded protein, wherein the host cells are present in an addressable array; and

(c) individually screening the sets of encoded proteins, whereby ~~to identify~~ one or more proteins that have ~~activity~~ a predetermined property that differs from the target protein are identified, wherein:

each such protein is designated a hit;

each hit contains a mutation designated a hit position; and

the predetermined property is selected from among chemical, physical and biological property of the target protein.

2. (original) The process of claim 1, wherein each set of nucleic acid molecules is individually designed and synthesized.

3. (original) The process of claim 2, wherein each set is deposited at a locus in an addressable array.

4. (original) The process of claim 1, wherein each polynucleotide in a set encodes a protein that differs by at least one amino acid from the target protein.

5. (original) The process of claim 1, wherein the array comprises a solid support with loci for containing or retaining cells; and each locus contains one set of cells.

6. (original) The process of claim 1, wherein the array comprises a solid support with wells for containing or retaining cells; and each well contains one set of cells.

7. (original) The process of claim 1, wherein the nucleic acid molecules comprise viral vectors; and the cells are eukaryotic cells that are transduced with the vectors.

8. (original) The process of claim 1, wherein the nucleic acid molecules comprise plasmids and the cells are bacterial cells.

9. (Currently amended) The method of claim 1, further comprising:

(d) modifying the nucleic acid molecules that encode the hits[[,]] to produce a set of nucleic acid molecules that encode modified hits;

(e) introducing the each set of nucleic acids that encode the modified hits into cells; and

(f) individually screening the sets of cells that contain the nucleic acid molecules that encode the modified hits to identify one or more cells that encodes a protein that has ~~activity~~ a predetermined property that differs from the target protein and has properties that differ from the original hits, wherein each such protein is designated a lead.

10. (original) The process of claim 9, wherein each set nucleic acid molecules in step (d) is individually designed and synthesized.

11. (original) The method of claim 1, wherein the nucleic acid molecules in step (a) are produced by a method selected from among nucleic acid shuffling, recombination, site-directed or random mutagenesis and *de novo* synthesis.

12. (original) The method of claim 9, wherein the nucleic acid molecules in step (d) are produced by a method selected from among nucleic acid shuffling, recombination, site-directed or random mutagenesis, and *de novo* synthesis.

13. (previously presented) The method of claim 2, wherein the nucleic acid molecules in step (a) are produced by systematically changing each codon in the target protein to a pre-selected codon.

14. (previously presented) the method of claim 13, wherein the codon is selected from a codon encoding Ala (A), Ser (S), Pro (P), or Gly (G).

15. The method of claim 13, wherein the codon is selected from a codon encoding Arg (R), Asn (N), Asp (D), Cys (C), Gln (Q), Glu (E), His (H), Ile (I), Leu (L), Lys (K), Met (M), Phe (F), Thr (T), Trp (W), Tyr (Y) or Val (V).

16. (Currently amended) The method of claim 9, wherein the nucleic acids of step (d) are produced by systematically replacing each codon that is a hit position, with a codon encoding ~~the remaining~~ another amino ~~acids~~ acid, to produce nucleic acid molecules each differing by at least one codon and encoding modified hits to identify leads.

17. (Currently amended) The method of claim 9, further comprising:

recombining the nucleic acid molecules encoding the leads;

introducing those nucleic acid molecules into cells; and

screening the cells to identify nucleic acid molecules that encode

optimized leads, where an optimized lead comprises two or more hit positions.

18. (original) The method of claim 17, wherein the recombining is two, three or more up to all of the nucleic acids encoding the leads.

19. (original) The method of claim 17, wherein the recombining is effected by a method selected from among nucleic acid shuffling, recombination, site-directed or random mutagenesis and *de novo* synthesis.

20. (original) The method of claim 1, wherein the modifications are effected in a selected domain of the target protein.

21. (original) The method of claim 1, wherein the modifications are effected along the full length of the target protein.

22. (Currently amended) The method of claim 1, wherein the change in a predetermined property comprises a change in an activity of the target protein that is at least about 10%, 20%, 30%, 40% or 50% compared to the unmodified target protein.

23. (Currently amended) The method of claim 1, wherein the change in the predetermined property comprises a change in an activity of the target protein that is at least about 75%, 100%, 200%, 500% or 1000% compared to the unmodified target protein.

24. (previously presented) The method of claim 7, wherein at step (b) the titer of the viral vectors in each set of cells is assessed.

25. (original) The method of claim 24, wherein titering is effected by real time virus titering, comprising:

(i) incubating the nucleic acid molecules or a vector (biological agent) comprising the nucleic acid molecules at an initial concentration C, which is the unknown titer, with the host cells at a constant known concentration, D;

(ii) measuring at successive times, an output signal, i;

(iii) determining the time $t\beta$, wherein:

$t\beta$ corresponds to $i=\beta$;

$\beta_{min} < \beta < \beta_{max}$;

$\beta_{min}$ and $\beta_{max}$ correspond to values of i at the inflection point of the curve $i=f(t)$, for the minimal and maximal values, respectively, of the concentrations of a reference biological agent for which the curve $t\beta=f(c)$ is predetermined; and

(iv) determining the initial concentration C.

26. (original) The method of claim 24, wherein titering is effected by Tagged Replication and Expression Enhancement, comprising:

(i) incubating with host cells a reporter virus vector with a titering virus of unknown titer, wherein the titering virus increases or decreases the output signal from the reporter virus; and

(ii) measuring the output signal of the reporter virus and determining the titer of the reporter virus;

(ii) determining the titer of the interfering virus by comparing the titer of the reporter virus in the presence and absence of the interfering virus.

27. (original) The process of claim 9, wherein the nucleic acid molecules comprise viral vectors; and the cells are eukaryotic cells that are transduced with the vectors.

28. (previously presented) The method of claim 27, wherein at step (f) the titer of the viral vectors in each set of cells is determined.

29. (original) The method of claim 28, wherein the target protein is a protein involved in viral replication.

30. (original) The method of claim 1, wherein the performance of the screened proteins is evaluated by a Hill analysis or by fitting the output signal to a curve representative of the interaction of the target protein and a test compound.

31. (previously presented) The method of claim 30, wherein the Hill analysis, comprises:

(a) preparing a sample of each nucleic acid molecule or a plasmid or vector that comprises each nucleic acid molecule (biological agent), wherein each sample is obtained by a serial dilution of the molecules or vector or plasmid at a concentration R1,

(b) incubating each sample of the dilution obtained in (a) with the host cells (target cells) at a constant concentration R2,

(c) determining a P product from the reaction R1 + R2, at a t moment, in each the sample; and

(d) preparing a theoretical curve H from the experimental points R1 and P, for each biological agent by iterative approximation of parameters of the reaction R1 + R2 $\rightarrow$ P, at the t moment, in accordance with the equation:

$$P = P_{max} (\pi R1)^r / (\kappa + (\pi R1)^r) \qquad r=1,\ldots,n \quad (2)$$

in which:

R1 represents the biological agent concentration in a sample from the scale;

R2 is concentration of target cells (in vitro or in vivo)

P (output) represents the product from the reaction R1 + R2 at a t moment;

$P_{max}$ represents the reaction maximal capacity;

$\kappa$ represents, at a constant R2 concentration, the biological system for responding to the biological agent (resistance constant R2);

r represents a dependent coefficient of R1 and corresponds to the Hill coefficient; and

$\pi$ represents the intrinsic power of the R1 biological agent to induce a response in the biological system (P production at the t moment), and

(e) sorting the $\kappa$ and $\pi$ values obtained in (d) for each protein encoded by the nucleic acid molecules or plasmids or vectors and the cells, and then ranking according to the values thereof.

32. (original) The process of claim 1 that is automated.

33. (original) The process of claim 32 that is computer-controlled.

34-41. (Cancelled)

42. (previously presented) The method of claim 13, wherein the nucleic acid molecules in step (a) are produced by systematically changing each codon one-by-one at a time in the target protein to a pre-selected codon, whereby each set of nucleic acid molecules encodes a protein that differs by only one amino acid from the target protein.

43. (previously presented) the method of claim 42, wherein the codon is selected from a codon encoding Ala (A), Ser (S), Pro (P), or Gly (G).

44. (previously presented) The method of claim 42, wherein the codon is selected from a codon encoding Arg (R), Asn (N), Asp (D), Cys (C), Gln (Q), Glu (E), His (H), Ile (I), Leu (L), Lys (K), Met (M), Phe (F), Thr (T), Trp (W), Tyr (Y) or Val (V).